

Dkt No.: 051501/0276397

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Carl Ware

Art Unit : 1644

Serial No. : 09/549,096

Examiner : Huynh, P.

Filed : April 12, 2000

Title : LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND METHODS OF USE

#11  
Harry  
Feb, 9, 02

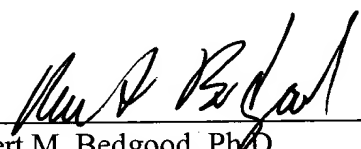
Commissioner for Patents  
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. §1.821(f) and (g)

The Sequence Listing in computer readable form is identical to the paper copy of the sequence listing submitted herewith. The sequence listing does not include new matter.

Respectfully submitted,

Date: 1-25-02

  
Robert M. Bedgood, Ph.D.  
Reg. No. 43,488

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

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**RAW SEQUENCE LISTING**  
**ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/549,096

Source: OPE

Date Processed by STIC: 7/5/2001

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**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

JAN 25 2002

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

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- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Please see RAW Sequence Report. Alternatively, Applicant should follow the format of the attached sample statement to request that the CRF filed in the parent application be used to create a CRF in this application.

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**



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## Raw Sequence Listing Error Summary

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ERROR DETECTEDSUGGESTED CORRECTION

SERIAL NUMBER: 09/549,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
    Wrapped Aminos    was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
    prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
    Numbering    use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
    ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
    each n or Xaa can only represent a single residue. Please present the maximum number of each  
    residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
    "bug"    sequences(s)         . Normally, PatentIn would automatically generate this section from the  
    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
    the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
    Artificial or Unknown sequences.
- 7      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
    (OLD RULES)    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i)    SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
    (NEW RULES)    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    (NEW RULES)    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
    Response    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
    is Artificial Sequence
- 11      Use of <220>    Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
    "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
    "bug"    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



Page 1 of 6  
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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/549,096

DATE: 07/05/2001  
TIME: 16:28:38

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\07032001\I549096.raw

Does Not Comply  
Corrected Diskette Needed

2 <110> APPLICANT: Ware, Carl F.  
4 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND METHODS  
OF USE  
6 <130> FILE REFERENCE: 051501/0276397  
8 <140> CURRENT APPLICATION NUMBER: 09/549,096  
9 <141> CURRENT FILING DATE: 2000-04-12  
11 <160> NUMBER OF SEQ ID NOS: 6  
13 <170> SOFTWARE: PatentIn Ver. 2.0

#### ERRORED SEQUENCES

61 <210> SEQ ID NO: 5  
62 <211> LENGTH: 1169  
63 <212> TYPE: DNA  
64 <213> ORGANISM: Homo sapiens  
66 <220> FEATURE:  
67 <221> NAME/KEY: CDS  
68 <222> LOCATION: (49)..(771)  
70 <400> SEQUENCE: 5  
71 gaggttgaag gaccagggcg tgtcagccct gctccagaga ccttgggc atg gag gag 57  
72 Met Glu Glu  
W--> 73  
74 agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc 105  
75 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile  
W--> 76 5 10 15  
W--> 77 ttc acg agg ctg gga cga agc cac cgg aga cag tgc tgc agt gtg 153  
E--> 78 Phe thr arg Leu gly arg ser his arg arg gln ser cys ser val  
W--> 79 25 30 35  
W--> 80 ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg 201  
E--> 81 gly Leu Leu Leu Leu Leu met gly ala gly Leu  
E--> 82 45 50  
E--> 83 gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag 249  
84 Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu  
W--> 85 55 60 65  
E--> 86 atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg 297  
87 Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu  
W--> 88 70 75 80  
E--> 89 ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca 345  
90 Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr  
W--> 91 85 90 95  
W--> 92 gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag 393  
E--> 93 ala asn ser ser Leu thr gly ser gly gly Pro Leu Leu trp glu  
W--> 94 105 110 115  
W--> 95 gcc ttc ctg agg ggc ctc agc tac cac gat ggg 441  
W--> 96 Ala Phe Leu Arg Gly Leu Ser Tyr His Asp Gly  
W--> 97 120 125 130  
E--> 98 gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg 489

DO NOT use  
TAB codes

↓  
move under respective  
codons

cca  
Pro  
20  
gcc cgg gtg ggt ctg  
Ala Arg Val Gly Leu  
40

What is  
this?

initial grouping  
of codons and amino  
acids

ggg  
Gly  
100  
act cag ctg ggc ctg  
Thr Gln Leu Gly Leu

also, see item 3 on Error Summary sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/549,096

DATE: 07/05/2001  
TIME: 16:28:38

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\07032001\I549096.raw

*Same  
even*

```

99 Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
W--> 100 135          140          145
E--> 101 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc 537
      102 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
W--> 103 150          155          160          cac ggc
W--> 104 ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg 585 His Gly
E--> 105 Leu tyr Lys arg thr Pro arg tyr Pro glu glu Leu glu Leu 165
W--> 106 170          175          ttg gtc agc cag cag tca
W--> 107 ccc tgc gga cgg gcc acc agc agc tcc cgg 633 Leu Val Ser Gln Gln Ser
E--> 108 Pro cys gly arg ala thr ser ser ser arg 180 185
W--> 109 190          195          gtc tgg tgg gac agc agc ttc ctg ggt ggt
W--> 110 gtg gta cac ctg gag gct 681 Val Trp Trp Asp Ser Ser Phe Leu Gly Gly
E--> 111 val val his Leu glu ala 200 205
E--> 112 210
E--> 113 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
      114 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
W--> 115 215          220          225
E--> 116 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga 771
      117 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
W--> 118 230          235          240
E--> 119 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc 831
E--> 120 aggggaaaga aaactcacga agcagaggct gggcgtgggt gctctcgct gtaatcccag 891
E--> 121 cactttggga ggccaaggca ggcggatcac ctgagggtcag gagttcgaga ccagcctggc 951
E--> 122 taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tgggtggtgcc 1011
E--> 123 tgcctgtaat ccagctaactc aggaggctga ggcaggataa ttttgcttaa acccgggagg 1071
E--> 124 cggaggttgc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
E--> 125 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1169
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 240
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
W--> 131 <400> SEQUENCE: 6
      132 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
      133 1 5 10 15
      134 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
E--> 135 20 25 30
      136 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
E--> 137 35 40 45
      138 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
E--> 139 50 55 60
      140 Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
E--> 141 70 75 80
      142 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
E--> 143 85 90 95
      144 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
E--> 145 100 105 110
      146 Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
E--> 147 115 120 125
      148 Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr

```

*misaligned  
amino acid nos.  
(see item 3 on  
Even summary  
sheet)*

Leu  
65

*misaligned  
grouping*

His Asp  
130

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/549,096

DATE: 07/05/2001

TIME: 16:28:38

Input Set A:\PTO.txt

Output Set N:\CRF3\07032001\I549096.raw

*same even*

```

E--> 149 135          140          Ser Lys Val Gln Leu Gly
      150 Gly Val Gly Cys Pro Leu Gly Leu Ala Ser          145          150
E--> 151 155          160          Thr Ile Thr His Gly Leu Tyr Lys Arg Thr
      152 Pro Arg Tyr Pro Glu Glu          165          170
E--> 153 175
      154 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
E--> 155 180          185          190
      156 Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
E--> 157 195          200          205          Leu Glu
      158 Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu          210
E--> 159 215          220          Val Arg Leu Arg Asp Gly
      160 Thr Arg Ser Tyr Phe Gly Ala Phe Met Val          225          230
E--> 161 235          240
      163 ATTORNEY DOCKET NO. 07246/030001
E--> 166 2

```

*delete at end of file*

*All sample Sequence Listings  
(attached) for val format*

*PS* Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.



**Attachment for PTO-948 (Rev. 03/01, or earlier)  
6/18/01**

**The below text replaces the pre-printed text under the heading, "Information on How to Effect Drawing Changes," on the back of the PTO-948 (Rev. 03/01, or earlier) form.**

**INFORMATION ON HOW TO EFFECT DRAWING CHANGES**

**1. Correction of Informalities – 37 CFR 1.85**

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the Notice of Allowability. Extensions of time may **NOT** be obtained under the provisions of 37 CFR 1.136(a) or (b) for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

**2. Corrections other than Informalities Noted by Draftsperson on form PTO-948.**

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

**Timing of Corrections**

Applicant is required to submit the drawing corrections within the time period set in the attached Office communication. See 37 CFR 1.85(a).

Failure to take corrective action within the set period will result in **ABANDONMENT** of the application.